

SEQUENCE LISTING

<110> Rothschild, Max
Ciobanu, Dan
Malek, Massoud
Plastow, Graham

<120> Novel PRKAG3 Alleles and Use of the Same as Genetic Markers for Reproductive and Meat Quality Traits

<130> P04668US3

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<151> 2000-09-08

<150> 60/260,239

<151> 2001-01-08

<150> 60/299,111

<151> 2001-06-18

<160> 17

<170> PatentIn version 3.0

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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
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ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
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Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
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Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
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PatentIn version 3.0

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Ser	Arg	Trp	Thr	Arg	Gln	Glu	Asp	Val	Glu	Glu	Gly	Gly	Pro	Pro	Gly	35	40	45	
Pro	Arg	Glu	Gly	Pro	Gln	Ser	Arg	Pro	Val	Ala	Glu	Ser	Thr	Gly	Gln	50	55	60	
Glu	Ala	Thr	Phe	Pro	Lys	Ala	Thr	Pro	Leu	Ala	Gln	Ala	Ala	Pro	Leu	65	70	75	80
Ala	Glu	Val	Asp	Asn	Pro	Pro	Thr	Glu	Arg	Asp	Ile	Leu	Pro	Ser	Asp	85	90	95	
Cys	Ala	Ala	Ser	Ala	Ser	Asp	Ser	Asn	Thr	Asp	His	Leu	Asp	Leu	Gly	100	105	110	
Ile	Glu	Phe	Ser	Ala	Ser	Ala	Ala	Ser	Gly	Asp	Glu	Leu	Gly	Leu	Val	115	120	125	
Glu	Glu	Lys	Pro	Ala	Pro	Cys	Pro	Ser	Pro	Glu	Val	Leu	Leu	Pro	Arg	130	135	140	
Leu	Gly	Trp	Asp	Asp	Glu	Leu	Gln	Lys	Pro	Gly	Ala	Gln	Val	Tyr	Met	145	150	155	160
His	Phe	Met	Gln	Glu	His	Thr	Cys	Tyr	Asp	Ala	Met	Ala	Thr	Ser	Ser	165	170	175	
Lys	Leu	Val	Ile	Phe	Asp	Thr	Met	Leu	Glu	Ile	Lys	Lys	Ala	Phe	Phe	180	185	190	2
Ala	Leu	Val	Ala	Asn	Gly	Val	Arg	Ala	Ala	Pro	Leu	Trp	Asp	Ser	Lys	195	200	205	
Lys	Gln	Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Leu	Val	210	215	220	
Leu	His	Arg	Tyr	Tyr	Arg	Ser	Pro	Leu	Val	Gln	Ile	Tyr	Glu	Ile	Glu	225	230	235	240

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
18-24	20.5 (2.5)
25-34	29.5 (4.5)
35-44	39.5 (5.5)
45-54	49.5 (6.5)
55-64	59.5 (7.5)
65-74	69.5 (8.5)
75-84	79.5 (9.5)
85-94	89.5 (10.5)
95-104	99.5 (11.5)
105-114	109.5 (12.5)
115-124	119.5 (13.5)
125-134	129.5 (14.5)
135-144	139.5 (15.5)
145-154	149.5 (16.5)
155-164	159.5 (17.5)
165-174	169.5 (18.5)
175-184	179.5 (19.5)
185-194	189.5 (20.5)
195-204	199.5 (21.5)
205-214	209.5 (22.5)
215-224	219.5 (23.5)
225-234	229.5 (24.5)
235-244	239.5 (25.5)
245-254	249.5 (26.5)
255-264	259.5 (27.5)
265-274	269.5 (28.5)
275-284	279.5 (29.5)
285-294	289.5 (30.5)
295-304	299.5 (31.5)
305-314	309.5 (32.5)
315-324	319.5 (33.5)
325-334	329.5 (34.5)
335-344	339.5 (35.5)
345-354	349.5 (36.5)
355-364	359.5 (37.5)
365-374	369.5 (38.5)
375-384	379.5 (39.5)
385-394	389.5 (40.5)
395-404	399.5 (41.5)
405-414	409.5 (42.5)
415-424	419.5 (43.5)
425-434	429.5 (44.5)
435-444	439.5 (45.5)
445-454	449.5 (46.5)
455-464	459.5 (47.5)
465-474	469.5 (48.5)
475-484	479.5 (49.5)
485-494	489.5 (50.5)
495-504	499.5 (51.5)
505-514	509.5 (52.5)
515-524	519.5 (53.5)
525-534	529.5 (54.5)
535-544	539.5 (55.5)
545-554	549.5 (56.5)
555-564	559.5 (57.5)
565-574	569.5 (58.5)
575-584	579.5 (59.5)
585-594	589.5 (60.5)
595-604	599.5 (61.5)
605-614	609.5 (62.5)
615-624	619.5 (63.5)
625-634	629.5 (64.5)
635-644	639.5 (65.5)
645-654	649.5 (66.5)
655-664	659.5 (67.5)
665-674	669.5 (68.5)
675-684	679.5 (69.5)
685-694	689.5 (70.5)
695-704	699.5 (71.5)
705-714	709.5 (72.5)
715-724	719.5 (73.5)
725-734	729.5 (74.5)
735-744	739.5 (75.5)
745-754	749.5 (76.5)
755-764	759.5 (77.5)
765-774	769.5 (78.5)
775-784	779.5 (79.5)
785-794	789.5 (80.5)
795-804	799.5 (81.5)
805-814	809.5 (82.5)
815-824	819.5 (83.5)
825-834	829.5 (84.5)
835-844	839.5 (85.5)
845-854	849.5 (86.5)
855-864	859.5 (87.5)
865-874	869.5 (88.5)
875-884	879.5 (89.5)
885-894	889.5 (90.5)
895-904	899.5 (91.5)
905-914	909.5 (92.5)
915-924	919.5 (93.5)
925-934	929.5 (94.5)
935-944	939.5 (95.5)
945-954	949.5 (96.5)
955-964	959.5 (97.5)
965-974	969.5 (98.5)
975-984	979.5 (99.5)
985-994	989.5 (100.5)
995-1004	999.5 (101.5)
1005-1014	1009.5 (102.5)
1015-1024	1019.5 (103.5)
1025-1034	1029.5 (104.5)
1035-1044	1039.5 (105.5)
1045-1054	1049.5 (106.5)
1055-1064	1059.5 (107.5)
1065-1074	1069.5 (108.5)
1075-1084	1079.5 (109.5)
1085-1094	1089.5 (110.5)
1095-1104	1099.5 (111.5)
1105-1114	1109.5 (112.5)
1115-1124	1119.5 (113.5)
1125-1134	

6

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ctg Leu	cac His	cgc Arg	tat Tyr	tac Tyr	agg Arg	tcc Ser	ccc Pro	ctg Leu	gtc Val	cag Gln	atc Ile	tac Tyr	gag Glu	att Ile	gaa Glu	720
225			230			235						240				
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245			250			255						255				
aag Lys	cct Pro	ctg Leu	gtc Val	tcc Ser	atc Ile	tct Ser	ccc Pro	aat Asn	gac Asp	agc Ser	ctg Leu	ttc Phe	gaa Glu	gct Ala	gtc Val	816
260			265			270						270				
tac Tyr	gcc Ala	ctc Leu	atc Ile	aag Lys	aac Asn	cgg Arg	atc Ile	cac His	cgc Arg	ctg Leu	ccg Pro	gtc Val	ctg Leu	gac Asp	cct Pro	864
275			280			285						285				
gtc Val	tcc Ser	ggg Gly	gct Ala	gtg Val	ctc Leu	cac His	atc Ile	ctc Leu	aca Thr	cat His	aag Lys	cgg Arg	ctt Leu	ctc Leu	aag Lys	912
290			295			300						300				
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305			310			315						320				
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325			330			335						335				
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355			360			365						365				
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370			375			380						380				
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385			390			395						400				
ctg Leu	tgt Cys	ctg Leu	gaa Glu	ggc Gly	gtc Val	ctt Leu	tcc Ser	tgc Cys	cag Gln	ccc Pro	cac His	gag Glu	acc Thr	ttg Leu	ggg Gly	1248
405			410			415						415				
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420			425			430						430				
gtg Val	gat Asp	gag Glu	acc Thr	cag Gln	cac His	ctt Leu	ctg Leu	ggc Gly	gtg Val	gtg Val	tcc Ser	ctc Leu	tct Ser	gac Asp	atc Ile	1344

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Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala			
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Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp			
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Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly			
100 105 110			

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
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Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

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Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp	
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Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly	
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Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val	
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Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg	
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His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
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Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	
180 185 190	
gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag	624
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys	
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Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	
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Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
225 230 235 240	
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc	768
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
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aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc	816
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	
260 265 270	
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct	864
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	
275 280 285	
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag	912
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys	
290 295 300	
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac	960
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr	

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Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val	325	330	335	
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac				1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp	340	345	350	
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg				1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val	355	360	365	
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca				1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr	370	375	380	
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca				1200
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr	385	390	395	400
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg				1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly	405	410	415	
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc				1296
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu	420	425	430	
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc				1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile	435	440	445	
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc				1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala	450	455	460	
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga				1452
gccgtggact cagctctcac ttccctcag cccacttgc tggctctggct cttgttcagg				1512
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gaaatctacc agcatcaaga ctactgtgg gaccactgct ttgtcccatt ctcagctgaa				1692
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g				1873
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
35 40 45

Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala

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455

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<213> Sus scrofa

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10

15

gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala

20

25

30

tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly

35

40

45

ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln

50

55

60

gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg 240

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu

65

70

75

80

gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac 288

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp

85

90

95

tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc 336

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly

100

105

110

ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg 384

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val

115

120

125

gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg 432

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg

130

135

140

ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg 480

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met

145

150

155

160

cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc 528

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser

165

170

175

aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt 576

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe

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gcc ctg gtg gcc aac ggc atc cga gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205			624
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220			672
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240			720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255			768
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val 260 265 270			816
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro 275 280 285			864
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys 290 295 300			912
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr 305 310 315 320			960
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val 325 330 335			1008
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp 340 345 350			1056
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val 355 360 365			1104
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr 370 375 380			1152
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr 385 390 395 400			1200
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly 405 410 415			1248
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc			1296

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu	
420 425 430	
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc	1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile	
435 440 445	
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc	1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala	
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gccgtggact cagctctcac ttcccctcag cccacttgc tgggtctggct cttgttcagg	1512
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gaaatctacc agcatcaaga ctactgtgg gaccactgct ttgtcccatt ctcagctgaa	1692
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35 40 45	
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln	
50 55 60	
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu	
65 70 75 80	
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp	
85 90 95	

325

330

335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
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Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
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Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
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<211> 1873
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gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30

tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
35 40 45

ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln

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gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp 85 90 95	288		
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly 100 105 110	336		
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val 115 120 125	384		
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg 130 135 140	432		
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met 145 150 155 160	480		
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser 165 170 175	528		
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe 180 185 190	576		
gcc ctg gtg gcc aac ggc gtc caa gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205	624		
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220	672		
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240	720		
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255	768		
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val 260 265 270	816		
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro 275 280 285	864		
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag	912		

Val	Ser	Gly	Ala	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys	
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Phe	Leu	His	Ile	Phe	Gly	Thr	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr	
305					310					315					320	
cgc	acc	atc	caa	gat	ttg	ggc	atc	ggc	aca	ttc	cga	gac	ttg	gcc	gtg	1008
Arg	Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val	
				325					330						335	
gtg	ctg	gaa	acg	gcg	ccc	atc	ctg	acc	gca	ctg	gac	atc	ttc	gtg	gac	1056
Val	Leu	Glu	Thr	Ala	Pro	Ile	Leu	Thr	Ala	Leu	Asp	Ile	Phe	Val	Asp	
				340					345						350	
cgg	cgt	gtg	tct	gcg	ctg	cct	gtg	gtc	aac	gaa	act	gga	cag	gta	gtg	1104
Arg	Arg	Val	Ser	Ala	Leu	Pro	Val	Val	Asn	Glu	Thr	Gly	Gln	Val	Val	
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ggc	ctc	tac	tct	cgc	ttt	gat	gtg	atc	cac	ctg	gct	gcc	caa	caa	aca	1152
Gly	Leu	Tyr	Ser	Arg	Phe	Asp	Val	Ile	His	Leu	Ala	Ala	Gln	Gln	Thr	
		370				375					380					
tac	aac	cac	ctg	gac	atg	aat	gtg	gga	gaa	gcc	ctg	agg	cag	cgg	aca	1200
Tyr	Asn	His	Leu	Asp	Met	Asn	Val	Gly	Glu	Ala	Leu	Arg	Gln	Arg	Thr	
385					390					395					400	
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Leu	Cys	Leu	Glu	Gly	Val	Leu	Ser	Cys	Gln	Pro	His	Glu	Thr	Leu	Gly	
				405						410					415	
gaa	gtc	att	gac	cgg	att	gtc	cgg	gaa	cag	gtg	cac	cgc	ctg	gtg	ctc	1296
Glu	Val	Ile	Asp	Arg	Ile	Val	Arg	Glu	Gln	Val	His	Arg	Leu	Val	Leu	
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gtg	gat	gag	acc	cag	cac	ctt	ctg	ggc	gtg	gtg	tcc	ctc	tct	gac	atc	1344
Val	Asp	Glu	Thr	Gln	His	Leu	Leu	Gly	Val	Val	Ser	Leu	Ser	Asp	Ile	
			435				440					445				
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Leu	Gln	Ala	Leu	Val	Leu	Ser	Pro	Ala	Gly	Ile	Asp	Ala	Leu	Gly	Ala	
			450				455					460				
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 <213> Sus scrofa

<400> 10

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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
 35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
 50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
 65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
 85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
 100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
 115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
 130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
 145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
 165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
 180 185 190

Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys

195

200

205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
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Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
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 <212> DNA
 <213> Sus scrofa

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